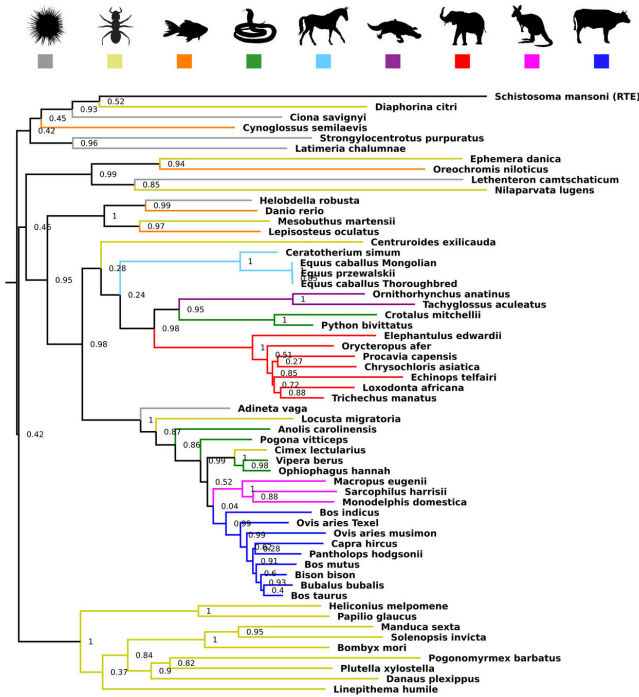


Cross species transfer of genes has driven evolution

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A graphic representation of the BovB element which shows how it has appeared in species that are wide apart on the evolutionary tree -- for example sea urchins and elephants, cows and snakes. Credit: University of Adelaide

Far from just being the product of our parents, University of Adelaide scientists have shown that widespread transfer of genes between species has radically changed the genomes of today's mammals, and been an important driver of evolution.

In the world's largest study of so-called "jumping genes", the researchers have traced two particular jumping genes across 759 species of plants, animals and fungi. These jumping genes are actually small pieces of DNA that can copy themselves throughout a [genome](#) and are known as transposable elements.

They have found that cross-species transfers, even between plants and animals, have occurred frequently throughout evolution.

Both of the transposable elements they traced—L1 and BovB—entered mammals as foreign DNA. This is the first time anyone has shown that the L1 [element](#), important in humans, has jumped between species.

"Jumping genes, properly called retrotransposons, copy and paste themselves around genomes, and in genomes of other species. How they do this is not yet known although insects like ticks or mosquitoes or possibly viruses may be involved—it's still a big puzzle," says project leader Professor David Adelson, Director of the University of Adelaide's Bioinformatics Hub.

"This process is called horizontal [transfer](#), differing from the normal parent-offspring transfer, and it's had an enormous impact on mammalian evolution."

For example, Professor Adelson says, 25% of the genome of cows and sheep is derived from jumping genes.

"Think of a jumping gene as a parasite," says Professor Adelson. "What's in the DNA is not so important—it's the fact that they introduce themselves into other genomes and cause disruption of genes and how they are regulated."

Published today in the journal *Genome Biology*, in collaboration with the South Australian Museum, the researchers found [horizontal gene transfer](#) was much more widespread than had been thought.

"L1 elements were thought to be inherited only from parent to offspring," says lead author Dr. Atma Ivancevic, postdoctoral researcher in the University of Adelaide's Medical School. "Most studies have only looked at a handful of species and found no evidence of transfer. We looked at as many species

as we could."

L1 elements in humans have been associated with cancer and neurological disorders. The researchers say that understanding the inheritance of this element is important for understanding the evolution of diseases.

The researchers found L1s are abundant in plants and animals, although only appearing sporadically in fungi. But the most surprising result was the lack of L1s in two key mammal species—the Australian monotremes (platypus and echidna) - showing that the gene entered the mammalian evolutionary pathway after the divergence from monotremes.

"We think the entry of L1s into the mammalian genome was a key driver of the rapid evolution of mammals over the past 100 million years," says Professor Adelson.

The team also looked at the transfer of BovB elements between species. BovB is a much younger jumping gene: it was first discovered in cows, but has since been shown to jump between a bizarre array of animals including reptiles, elephants and marsupials. Earlier research, led by Professor Adelson, found that ticks were the most likely facilitators of cross-species BovB transfer.

The new research extended the analysis to find that BovB has jumped even more widely than previously anticipated. BovB has transferred at least twice between frogs and bats, and new potential vector species include bed bugs, leeches and locusts.

The team believes that studying insect species will help find more evidence of cross-species transfer. They also aim to study other jumping genes and explore the possibility of aquatic vectors, such as sea worms and nematodes.

"Even though our recent work involved the analysis of genomes from over 750 species, we have only begun to scratch the surface of horizontal gene transfer," says Professor Adelson. "There are many more [species](#) to investigate and other types of jumping [genes](#)."

More information: Atma M. Ivancevic et al,

Horizontal transfer of BovB and L1 retrotransposons in eukaryotes, *Genome Biology* (2018). [DOI: 10.1186/s13059-018-1456-7](https://doi.org/10.1186/s13059-018-1456-7)

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